STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/561,504*
Source: *IFWP*
Date Processed by STIC: *12/29/05*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , **EFS Submission User Manual - ePAVE**)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (**EFFECTIVE 01/14/05**): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: _10/561,504_ |

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length
The rules require that a line **not exceed 72 characters** in length. This includes white spaces.

3 _____ Misaligned Amino Numbering
The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4 _____ Non-ASCII
The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10 _____ Invalid <213> Response
Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n/Xaa
"n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

IFW

```
          RAW SEQUENCE LISTING            DATE: 12/29/2005
          PATENT APPLICATION:  US/10/561,504     TIME: 15:04:31

          Input Set : A:\304561_Sequence_Listing.txt
          Output Set: N:\CRF4\12292005\J561504.raw

       3 <110> APPLICANT: Tamai, Ikumi
       4         Nozawa, Takashi
       6 <120> TITLE OF INVENTION: Screening Method for Therapeutic Agent for Breast Cancer
       8 <130> FILE REFERENCE: 051009/304561
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/561,504
C--> 11 <141> CURRENT FILING DATE: 2005-12-19
      13 <160> NUMBER OF SEQ ID NOS: 22
      15 <170> SOFTWARE: PatentIn version 3.1
```

ERRORED SEQUENCES

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     269 <210> SEQ ID NO: 22
     270 <211> LENGTH: 20
     271 <212> TYPE: DNA
     272 <213> ORGANISM: Artificial
     274 <220> FEATURE:
     275 <223> OTHER INFORMATION: (AT4)
     277 <400> SEQUENCE: 22
     278 gagattggaa cccagtctct
E--> 282 5
E--> 285 5
E--> 287 rta01/2195262v1
E--> 289 rta01/2195262v1
```

*Does Not Comply
Corrected Diskette Needed*

insufficient explanation
(give source of genetic material)
20
(see item 11
on Error Summary Sheet)

delete
at end of file

see p.2

SEQUENCE LISTING

<110> Tamai, Ikumi
      Nozawa, Takashi

These are prior data

<120> Screening Method for Therapeutic Agent for Breast Cancer

<130> 051009/304561

</1507 <140> JP2003-177021
</1517 <141> 2003-06-20

<160> 22

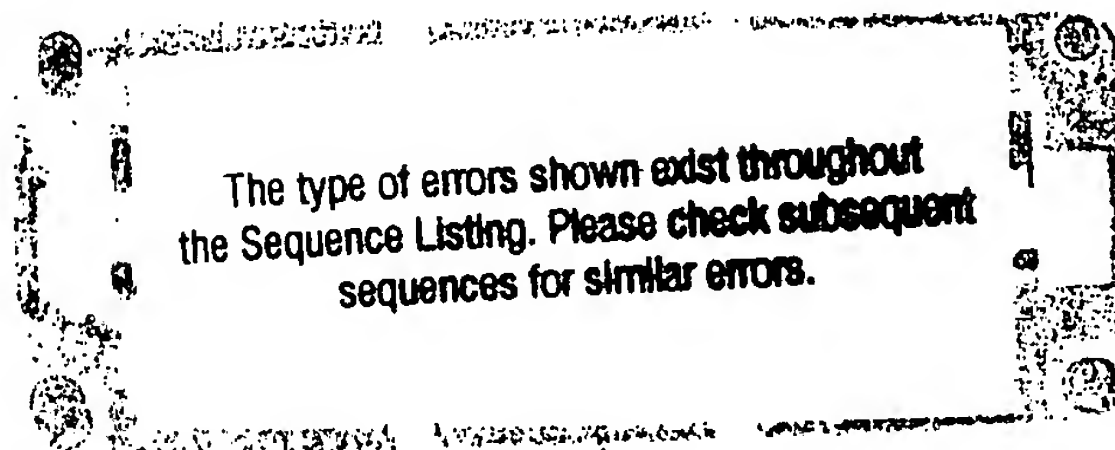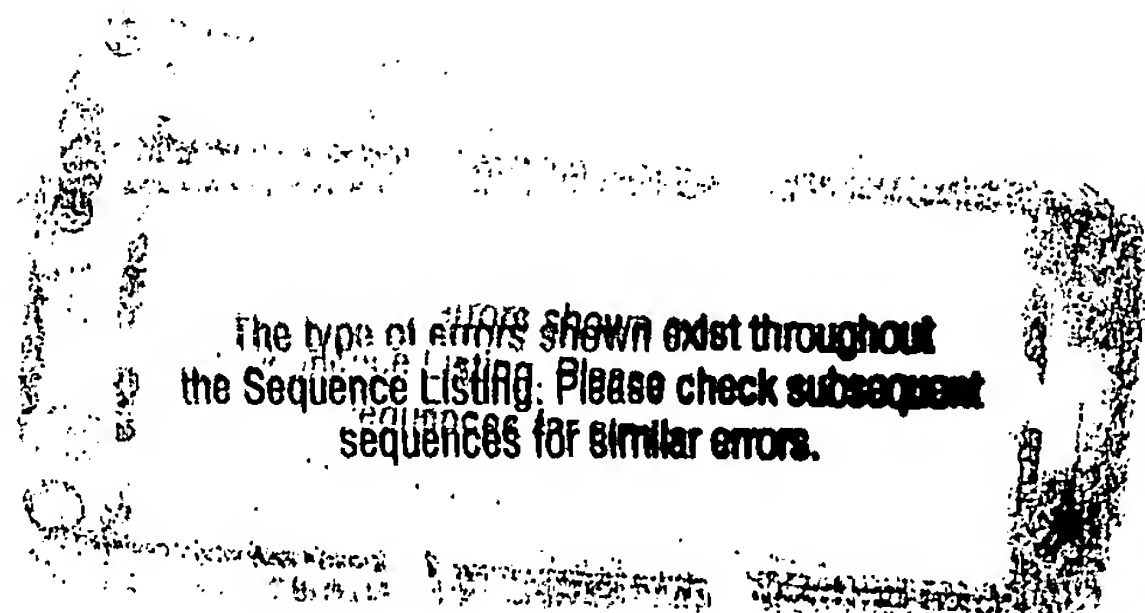<170> PatentIn version 3.1

<210> 1
<211> 20
<212> DNA
<213> Artificial

<220>
<223> ATP-A   *another example of an insufficient explanation for <213> Artificial*

<400> 1
aaacaagctg cccacatagg   20

(global error)

VERIFICATION SUMMARY   DATE: 12/29/2005
PATENT APPLICATION: US/10/561,504   TIME: 15:04:32

Input Set : **A:\304561_Sequence_Listing.txt**
Output Set: **N:\CRF4\12292005\J561504.raw**

```
L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:282 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:285 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:287 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:25 SEQ:22
L:287 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:10
L:287 M:112 C: (48) String data converted to lower case,
L:289 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:30 SEQ:22
L:289 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:10
L:289 M:112 C: (48) String data converted to lower case,
L:289 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:30 SEQ:22
```